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## Somatic mutations of the immunoglobulin framework are generally required for broad and potent HIV-1 neutralization

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### Summary

Broadly neutralizing antibodies to HIV-1 (bNAbs) can prevent infection and are therefore of great importance for HIV-1 vaccine design. Notably, bNAbs are highly somatically mutated and generated by a fraction of HIV-1-infected individuals several years after infection. Antibodies typically accumulate mutations in the complementarity determining region (CDR) loops, which usually contact the antigen. The CDR loops are scaffolded by canonical framework regions (FWRs) that are both resistant to and less tolerant of mutations. Here we report that in contrast to most antibodies, including those with limited HIV-1 neutralizing activity, most bNAbs require somatic mutations in their FWRs. Structural and functional analyses reveal that somatic mutations in FWR residues enhance breadth and potency by providing increased flexibility and/or direct antigen contact. Thus, in bNAbs, FWRs play an essential role beyond scaffolding the CDR loops and their unusual contribution to potency and breadth should be considered in HIV-1 vaccine design.

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## Introduction

A fraction of HIV-1-infected individuals mount a broadly neutralizing serologic response (Doria-Rose et al., 2010; Simek et al., 2009) 2–3 years after infection (Mikell et al., 2011). Antibodies generated by these individuals are of great interest for vaccine design because they can protect macaques from infection (Mascola et al., 2000; Moldt et al., 2012; Shibata et al., 1999). Moreover, combinations of broadly neutralizing antibodies can control an established HIV-1 infection in humanized mice (Klein et al., 2012b).

Despite their potential importance to vaccine development and HIV-1 therapy, little was known about the molecular composition of the human anti-HIV-1 antibody response until single cell antibody cloning techniques were developed and used for characterizing IgGs from the sera of HIV-1-infected individuals with broadly neutralizing activity (Scheid et al., 2009a; Scheid et al., 2009b). This analysis revealed highly potent bNAbs, all of which might eventually be used in vaccine development (Corti et al., 2010; Huang et al., 2012; Morris et al., 2011; Mouquet et al., 2012; Scheid et al., 2011; Walker et al., 2009; Walker et al., 2011b; Wu et al., 2010).

A surprising observation was that anti-HIV-1 antibodies are highly somatically mutated when compared to other immunoglobulins (IgGs) cloned from the same patients (Scheid et al., 2009a; Xiao et al., 2009a; Xiao et al., 2009b). Whereas most human antibodies that have undergone affinity maturation carry 15–20 somatic mutations (Tiller et al., 2007), potent broadly neutralizing antibodies carry 40–110 mutations (Corti et al., 2010; Scheid et al., 2011; Walker et al., 2009; Walker et al., 2011b; Wu et al., 2010; Xiao et al., 2009a; Xiao et al., 2009b). These mutations are essential because reversion to the antibody germline sequence drastically reduces neutralizing potency and breadth (Mouquet et al., 2010; Scheid et al., 2011; Wu et al., 2011; Xiao et al., 2009b; Zhou et al., 2010). However, why so many mutations appear to be required is not known.

Wu and Kabat first divided antibody variable regions into complementarity determining regions (CDRs) and framework regions (FWRs) based on the number of somatic hypermutations in these regions (Wu and Kabat, 1970) (Figure 1A, and B). The CDRs consist primarily of loops that form the sites of contact between the antibody and antigen (Amzel and Poljak, 1979), and account for the specificities of most antibody molecules as demonstrated by CDR grafting experiments (Jones et al., 1986). The structural integrity of the variable domains is maintained by the FWRs, which encode nine anti-parallel  $\beta$ -strands arranged into two  $\beta$ -sheets (one sheet containing strands A, B, E and D and the other containing strands C', C, F and G; Figure 1A and B). The relatively invariant  $\beta$ -strands of the FWRs serve as a scaffold for three CDR loops, which connect strands B and C, C' and C'', and F and G (Figure 1A and B) (Amzel and Poljak, 1979).

Somatic mutations are preferentially found in the CDR loops where they can alter the antibody combining site without affecting the overall structure of the variable domain (Wu and Kabat, 1970). Mutations in the FWR are usually poorly tolerated and generally biased to neutral substitutions to avoid changes that would destroy the structural underpinnings of the variable domain (Reynaud et al., 1995; Wagner et al 1995).

Here we examine the role of somatic mutations in the development of broadly neutralizing anti-HIV-1 antibodies. In contrast to most other antibodies, including anti-HIV-1 antibodies with limited neutralization activity, we found that FWR mutations, including non-contact residues, are essential for the neutralizing activity of most potent bNAbs. We propose that the requirement to alter the FWR, without destroying its essential structural elements,

accounts for the high mutation load found in broadly neutralizing anti-HIV-1 antibodies and possibly for the difficulty and prolonged latency with which such antibodies develop.

## Results

### Somatic Hypermutation in HIV-neutralizing Antibodies

To examine the role of somatic hypermutations in anti-HIV-1 antibody neutralization breadth and potency, we selected a group of 9 HIV-1-reactive antibodies with activity limited to easy to neutralize (Tier 1) HIV-1 strains (Seaman et al., 2009), and 17 antibodies with broad neutralization activity (Figure 1C, Figure S1 and Table S1). The antibodies with limited neutralizing activity included antibodies recognizing the CD4 binding site (CD4bs; 6–187, 9–913, 11–989) (Mouquet et al., 2011; Scheid et al., 2009a), the core epitope (1–479, 2–491, 11–591) (Mouquet et al., 2011; Pietzsch et al., 2010; Scheid et al., 2009a), the V3-loop (447–52D, 10–188) (Gorny et al., 1993; Mouquet et al., 2011) and the CD4-induced site (17b) (Thali et al., 1993) (Table S1). Eight of the 17 bNAbs also recognize the CD4bs (VRC01, NIH45–46, 3BNC60, 12A12, 1NC9, 8ANC131, 12A21, 3BNC117) (Scheid et al., 2011; Wu et al., 2010), whereas others recognized the V1/V2 loop (PG16) (Walker et al., 2009), carbohydrates (2G12) (Calarese et al., 2003; Trkola et al., 1996), the core epitope (HJ16) (Corti et al., 2010), the base of the V3-loop (10–1074, PGT128) (Mouquet et al., 2012; Walker et al., 2011a), the membrane proximal external region (MPER; 4E10, 2F5) (Buchacher et al., 1994; Muster et al., 1993) and two antibodies (3BC176 and 8ANC195) (Klein et al., 2012a; Scheid et al., 2011) for which the precise epitopes are not yet determined (Figure 1C and Table S1).

Antibodies with limited neutralizing activity differ from bNAbs in that they generally carry fewer somatic mutations (Figure 1C, Figure S1 and Table S1). We used the well accepted Kabat system (Wu and Kabat, 1970) that utilizes sequence comparisons for FWR/CDR assignments. However, direct comparisons between Kabat and the IMGT numbering system (Giudicelli et al., 2006) (Figure 1B), which includes antibody structural data, were also performed for a subset of antibodies.

Complete reversion of somatic mutations in the heavy and light chain V genes (FWR1–3 and CDR1/2) drastically reduces anti-HIV-1 antibody binding and neutralization activity (Buchacher et al., 1994; Mouquet et al., 2010; Scheid et al., 2011; Xiao et al., 2009b; Zhou et al., 2010). Moreover, reverting only the CDR1 and CDR2 in 3BNC60 and NIH45–46 strongly diminished binding and neutralization (Figure S2A, Supplementary Data 1A). To determine the functional consequences of FWR mutations, we reverted the framework residues to their germline counterparts (FWR-GL) in each of the 26 selected antibodies (Supplementary Data 1B–D) and evaluated binding to HIV-1 envelope proteins as well as their neutralization activities.

### HIV-1-reactive Antibodies with limited Activity

As expected, reversion of somatic mutations in the FWR residues (FWR-GL) of the HIV-1 antibodies with limited breadth had only minimal effects on binding of most of these antibodies to gp140<sup>YU2</sup> (Figure S2B) as measured by ELISA and confirmed by SPR (not shown). Only two of these FWR-GL antibodies (9–913 and 10–188) showed a decrease in binding (Figure S2B). In agreement with the ELISA and SPR experiments, we found little or no change in neutralizing activity in most of the FWR-GL antibodies with limited neutralization activity on a panel of up to 6 Tier 1 viruses representing clades A, B and C (Figure S2B and Table S2). Only antibodies 9–913 and 10–188, which displayed decreased binding to gp140<sup>YU2</sup>, showed a decrease (9–913) or complete loss (10–188) in neutralizing activity (Figure S2B and Table S2). We conclude that with two exceptions out of 9

antibodies tested, FWR mutations do not alter the binding or neutralizing activity of anti-HIV-1 antibodies with limited neutralizing activity. Thus, despite their significantly higher levels of somatic mutation, HIV-1 neutralizing antibodies with limited breadth resemble previously characterized antibodies to other antigens in that FWR mutations seem not to be essential.

### Potent Broadly Neutralizing Antibodies

In contrast, reversion of the FWR mutations in most of the 17 broadly neutralizing antibodies decreased their binding to gp140<sup>YU2</sup> (Figure 2 and Figure 3). Three of the antibodies, PG16 (Walker et al., 2009), 8ANC195 (Scheid et al., 2011) and 3BC176 (Klein et al., 2012a) bound poorly to gp140<sup>YU2</sup> when measured up to 8 µg/ml and differences in binding between mutated and reverted antibodies could not be evaluated (Figure 2).

The neutralizing activity of the reverted antibodies was tested on a panel of 11 viruses (Tier 1 to Tier 3) representing HIV-1 clades A, B and C (Figure 2, Figure 3 and Table S2). The majority of the FWR-GL antibodies lost nearly all their neutralizing activity against the tested strains. Similar results were also obtained when we produced FWR-GL antibody versions of VRC01, 3BNC60 and 8ANC131 according to IMGT alignment (Supplementary Data 1F, Figure S2C). 4E10, which is among the least potent antibodies of the bNAbs tested, was the exception to the rule in retaining binding to gp140<sup>YU2</sup> as well as potency and breadth. PG16 retained most of its neutralizing breadth, but like the other bNAbs, it lost potency by at least 10-fold after FWR reversion (geometric mean IC<sub>50</sub> values increased from 0.95 to 9.69, Figure 2 and Table S2). 2G12 represents a special case for interpreting the effects of FWR residue reversion because the two Fabs of 2G12 IgG form a domain-swapped (Fab)<sub>2</sub> unit that creates a single antigen binding site for recognizing a constellation of host-derived high mannose carbohydrates on gp120 (Calarese et al., 2003) (Figure S3). FWR residues are critical for the Fab dimerization via domain swapping (Huber et al., 2010) as well as for formation of a novel carbohydrate binding site at the V<sub>H</sub>-V<sub>H</sub>' interface (Calarese et al., 2003).

To provide a general understanding of the relationship between direct FWR contacts and CDRH3 length on the degree of FWR somatic mutation, we analyzed these parameters for bNAbs for which antibody-antigen structures have been determined. No correlation was observed with CDRH3 length and degree of heavy chain, light chain or total amount of FWR somatic mutation (Figure S4). Notably, however, the FWR contact surface area with antigen did correlate with the total number of amino acid changes in FWRs (Figure S4; *p*-value = 0.0088; rho=0.533).

To determine whether the effects of FWR reversion on binding and neutralization were simply due to alterations in contact residues, we selectively reverted all mutated FWR residues except for the contact residues (FWR-GL<sup>CR+</sup>; Figure 3) in 4 bNAbs whose contact residues were known (VRC01, NIH45-46, 12A21, 3BNC117) (Scheid et al., 2011; Wu et al., 2011; Zhou et al., 2010; Zhou et al., submitted). Despite retaining their FWR contact residues, all of the partially reverted antibodies showed lower levels of binding by ELISA and SPR. Interestingly, the SPR binding curves showed that loss of affinity appeared to be primarily due to an increased dissociation rate (off-rate; *k<sub>d</sub>*) (Figure 3). We conclude that FWR mutations enhance the affinity of broadly neutralizing antibodies primarily by decreasing the dissociation rate. Most importantly, FWR-GL<sup>CR+</sup> antibodies that retained somatically mutated FWR contact residues lost both neutralizing breadth and potency (Figure 3 and Table S2). We conclude that FWR mutations in non-contact residues are essential for the binding, breadth and potency of most broadly neutralizing anti-HIV-1 antibodies.

## Importance of a FWR insertion in 3BNC60

Insertions and deletions are infrequent by-products of somatic hypermutation that occur as a result of double-strand DNA breaks induced by deamination of neighboring cytidine residues by activation induced cytidine deaminase (AID) (Pavri and Nussenzweig, 2011; Wilson et al., 1998). Nevertheless, several potent anti-CD4bs antibodies, including 3BNC60, contain insertions within FWRs that are acquired during somatic mutation (Scheid et al., 2011). Sequence analysis of the clonal relatives of 3BNC60 (clone RU01) revealed a correlation between the presence of this insertion and neutralizing activity (Figure 4). Superimposition of the 3BNC60 Fab structure onto the Fab portion of the NIH45–46/gp120 complex structure (Diskin et al., 2011) suggested that this insertion might enhance binding by interacting with the V1/V2 loop region that was truncated in the gp120 construct that was crystallized (Figure 5A) (similar results were found when superimposing the 3BNC60 Fab onto the 3BNC117 Fab, two nearly identical antibodies, in the 3BNC117/gp120 co-crystal structure (Zhou et al., submitted)). To assess the effects of the insertion within FWR3 of the 3BNC60 heavy chain, we constructed a 3BNC60 mutant (3BNC60 I) in which the Trp-Asp-Phe-Asp insertion was removed (Figure 5B) and evaluated its neutralization activity against a panel of 7 viruses chosen to include strains that were resistant to VRC01 but sensitive to 3BNC60 (Figure 5C). 3BNC60AI lost neutralization potency against all 7 viruses. Adding the insertion to 3BNC55, a weaker variant of 3BNC60 isolated from the same donor (Scheid et al., 2011), increased the neutralization potency of 3BNC55+I compared to 3BNC55 against one viral strain (TRO.11) (Figure 5C). Addition of the insertion did not, however, restore the ability of a VRC01 plus insertion mutant to neutralize VRC01-resistant viruses (Supplementary Data 1E and Table S2). Taken together, these results demonstrate that the FWR insertion is critical for the neutralization activity of 3BNC60, but that its ability to improve potency requires a precise recognition geometry that is not always found in other potent anti-CD4bs antibodies.

## Crystal structure of a partially-reverted Fab

We previously noted a disruption in the canonical variable domain fold of the V<sub>H</sub> domain of 3BNC60 (Scheid et al., 2011); namely, the main chain hydrogen bonding pattern between strands C'' and C' was disrupted by the presence of Pro61 (Kabat numbering position 60; IMGT position 68) located at the C-terminal end of strand C'' (Figure 6A). In contrast, the germline V<sub>H</sub> sequence and other potent anti-CD4bs antibodies contain an alanine at this position (Scheid et al., 2011) (Supplementary Data 1C and D). A proline within a  $\beta$ -strand cannot form a main chain hydrogen bond with a carbonyl oxygen in an adjacent  $\beta$ -strand because it lacks a hydrogen atom attached to its mainchain nitrogen (Figure 6A). Nevertheless, this proline mutation is associated with increased antibody potency among clonal members of the 3BNC60 family (Figure 4) (Scheid et al., 2011).

Although classified by Kabat (Kabat et al., 1991) as part of CDRH2, residue 61 is within the C''  $\beta$ -strand of the Ig V domain fold and is classified as a FWR residue by IMGT (Lefranc et al., 1999) (Figure 1B, Figure S5). Thus we were interested in its potential role in antigen recognition. In the structure of the free 3BNC60 Fab, the region surrounding Pro61 is stabilized by a crystal contact (Figure S6) into a position that would clash with the CD4 binding loop of gp120 (Diskin et al., 2011; Scheid et al., 2011; Wu et al., 2011; Zhou et al., 2010). The potential clash with gp120 suggests that the region surrounding 3BNC60 Pro61 rearranges upon gp120 binding. Indeed, in the structure of a gp120 complex with the nearly identical antibody 3BNC117, the Fab exhibits a canonical V<sub>H</sub> domain structure in its gp120-bound conformation (Zhou et al., submitted) (Figure 6A). In addition, a murine Fab structure including a proline at this position shows minimal disruption of the  $\beta$ -sheet including strand C'' (Stanfield et al., 1990) (Figure 6A).



To address the unusual properties of the C'' strand in 3BNC60, we solved the 2.65 Å crystal structure of 3BNC60<sup>P61A</sup> (pdb code 4GW4), a single amino acid revertant mutant form of 3BNC60 (Figure 6A, Table S3). Like other Fabs containing alanine at position 61, including VRC01 (Zhou et al., 2010), VRC03, VRC-PG04 (Wu et al., 2011) and NIH45–46 (Diskin et al., 2011; Scheid et al., 2011), strand C'' of 3BNC60<sup>P61A</sup> Fab exhibited normal hydrogen bonding to the neighboring C' strand (Figure 6A). Although the displaced region of strand C'' in the 3BNC60 Fab was involved in interactions with a crystallographic neighbor, perhaps stabilizing it in the conformation observed in the structure (Scheid et al., 2011), the corresponding region of strand C'' in the 3BNC60<sup>P61A</sup> Fab did not contact a crystallographic neighbor despite isomorphous packing interactions in the 3BNC60 and 3BNC60<sup>P61A</sup> crystals (Figure S6).

To further evaluate the effects of the Pro to Ala substitution in strand C'', we compared the thermal stability of the 3BNC60 and 3BNC60<sup>P61A</sup> Fabs (Figure 6B). Both proteins exhibited denaturation profiles characteristic of two-state (native to denatured) unfolding, however the 3BNC60<sup>P61A</sup> Fab showed increased thermal stability compared with the wild-type 3BNC60 Fab, as demonstrated by a higher transition midpoint ( $T_m$ ) (Figure 6B).

The functional consequences of the Pro to Ala substitution were evaluated by comparing the neutralization potencies of 3BNC60 and 3BNC60<sup>P61A</sup> IgGs against 19 representative strains sensitive to 3BNC60 (Figure 6C). The substitution affected the neutralizing activity of the antibody against 7 of the strains (highlighted red; Figure 6C). We conclude that somatic mutation in the  $\beta$ -sheet framework involving strand C'' is essential for the potency and breadth of 3BNC60.

## Discussion

The  $\beta$ -sandwich structure of the immunoglobulin fold lends itself to a natural division into relatively structurally invariant  $\beta$ -strand FWRs and the more structurally diverse loops connecting the  $\beta$ -strands, three of which form the hypervariable CDRs (Figure 1A, B). Thus, mutations in FWRs are usually poorly tolerated and selected against, whereas mutations in the structurally diverse CDRs are well tolerated. Starting with the first crystal structure of a Fab bound to a protein antigen (Amit et al., 1986), antibody-antigen complex structures have confirmed that residues within the CDR loops usually form the majority of contacts with the antigen. Therefore the primary role of FWR residues is to provide a scaffold for the antigen-contacting CDRs, as evidenced by the common practice of CDR grafting (Jones et al., 1986). However, we find that in contrast to most antibodies, including HIV-1-reactive antibodies with limited neutralizing activity (Figure S1, S2B), somatically mutated FWR residues are critical for the breadth and potency of broadly neutralizing anti-HIV-1 antibodies (Figure 2 and Figure 3). Thus, the FWRs in these unusual antibodies serve an essential function beyond that of a scaffold for antigen-binding CDRs.

Understanding the excessive somatic hypermutation found in bNAbs requires consideration of the process by which antibodies are mutated. B cells undergo somatic hypermutation in germinal centers during T cell-dependent immune responses (Victora and Nussenzweig, 2011). The mutations are introduced by AID, which preferentially targets cytosines embedded in RGYW nucleotide sequences (in which R can be A or G, Y can be C or T, and W can be A or T) in antibody variable regions (Pavri and Nussenzweig, 2011). However, mutations are not limited to cytidine residues because error prone repair mechanisms also contribute to the repair of the initial lesions (Pavri and Nussenzweig, 2011; Peled et al., 2008). Thus, the mutation process is far more random than it would occur if only RGYW cytidines were targeted.

Mutations that enhance antibody affinity are rare, but they are positively selected in the germinal center as a result of increased antigen uptake and MHC-peptide presentation, which results in increased T cell-mediated help (Victoria and Nussenzweig, 2011). Mutations that increase antibody affinity can do so by increasing the on-rate or by decreasing the off-rate. The on-rate is diffusion limited, and the off-rate is limited by speed of antigen internalization because once the antigen is in a degradative endosome it will be digested irrespective of its rate of release from the antibody (Batista and Neuberger, 1998; Foote and Milstein, 1991). Thus, naturally developing antibody affinities do not normally exceed an affinity of  $10^{-11}$  M. In humans, this degree of affinity maturation is usually achieved with an average of 10–15 nucleotide mutations focused in the antigen contact residues in the CDR loops.

Although somatic mutations occur throughout the variable region, mutations that alter the amino acid coding sequence of the antibody accumulate preferentially in CDRs in part because of higher level of degeneracy of the codons used in the FWRs (Jolly et al., 1996; Reynaud et al., 1995; Wagner et al., 1995). Any alterations in the FWR are constrained by the fact that they must conserve the overall structure of the antibody because B cells that fail to express surface Ig are destined to die by apoptosis (Rajewsky, 1996). Indeed the FWRs appear to have evolved a nucleotide coding sequence that resists mutation in order to prevent changes in relatively invariant  $\beta$ -strands that are required to scaffold the CDR loops (Jolly et al., 1996; Reynaud et al., 1995; Wagner et al., 1995). Thus, a large number of random nucleotide mutations would be required to alter the FWR in a manner that optimizes the broadly neutralizing anti-HIV-1 antibodies while conserving essential structural elements.

The mutated FWR residues in the broadly neutralizing anti-HIV-1 antibodies contribute to binding and enhance breadth and potency in several different ways. In some cases, the substituted FWR residues directly contact the antigen; for example, crystal structures of the bNAbs VRC01 and NIH45–46 complexed with gp120 (Diskin et al., 2011; Zhou et al., 2010) reveal that FWR residue Arg71 in both VRC01 and NIH45–46 forms a salt bridge with gp120 residue Asp368. Thus, FWR mutation can serve to directly increase the binding interface by recruiting portions of the antibody that are not normally involved in antigen recognition. Moreover the ligand-bound structure of PGT128 (Pejchal et al., 2011) shows that the carbohydrate attached to Asn121<sub>gp120</sub> interacts with residues within the C'  $\beta$ -strand of the antibody heavy chain (Trp56, Thr57, His59 and Lys64). Two of these residues represent somatic mutations. In other cases, FWR residues do not appear to directly contact the antigen, yet are required for potency. For example, the FWRs of PG16 do not contribute substantially to direct antigen contacts and interaction with the antigen is mainly mediated through a long CDR3 loop (Pancera et al., submitted) (Figure S4).

Somatic mutation of residues within the  $\beta$ -sheet framework of the V domain can also indirectly affect the V domain structure so as to facilitate HIV-1 antigen recognition, as exemplified by the Pro61 residue in the broadly neutralizing antibodies 3BNC60/3BNC117 (Figure 6). Residue 61 falls within the  $\beta$ -sheet framework of the Ig V domain. Substitution of this proline to the germline alanine in 3BNC60 resulted in increased thermal stability, but a loss of neutralization activity against some HIV-1 strains. The structural effects of the proline to alanine substitution were revealed by comparison of the crystal structures of the 3BNC60<sup>P61A</sup> and 3BNC60 Fabs: the V<sub>H</sub> domain  $\beta$ -strand that was disrupted by the proline in the 3BNC60 structure was restored to its canonical position in the mutant Fab structure (Figure 6A). In the 3BNC117/gp120 structure (Zhou et al., submitted), the Pro61-containing  $\beta$ -strand is shifted from its position in the free 3BNC60 structure (where it was likely stabilized into the observed conformation by crystal packing forces) in order to avoid clashing with the CD4-binding loop in gp120, as predicted previously for 3BNC60/gp120

complexes (Scheid et al., 2011) (Figure 6A). The lower thermal stability of 3BNC60 Fab compared with 3BNC60<sup>P61A</sup> Fab (Figure 6B) is consistent with flexibility that would allow this sort of displacement.

Superimposition of the 3BNC60<sup>P61A</sup> Fab into the 3BNC117/gp120 co-crystal structure (Zhou et al., submitted) suggests that an alanine would be accommodated equally as well as a proline at position 61, and the fact that the P61A mutant of 3BNC60 neutralizes some HIV-1 strains equally as well as wildtype 3BNC60 suggests that Pro61 does not make any direct contacts to HIV-1 gp120 that are critical for binding to gp120 and neutralization. Instead we speculate that in the case of 3BNC60 and 3BNC117, the ability to disrupt the C' – C'' portion of the C'C''CFG  $\beta$ -sheet, which provides flexibility for V<sub>H</sub> residues 60–66, is necessary in order to accommodate antigenic sequence heterogeneity in or near the gp120 V5 loop. Taken together, these results provide a counterintuitive example of a neutral or functionally favorable somatic mutation that decreases the Fab stability by disrupting the canonical V<sub>H</sub> domain fold, allowing flexibility of the  $\beta$ -sheet framework that is needed for optimal antigen binding and neutralization (Figure 6C).

The high level of mutation found in broadly neutralizing antibodies would be difficult to explain in the context of an immune response to a conventional antigen and a single round of germinal center selection. However, HIV-1 differs from conventional antigens in that it presents the host with a continuously evolving target that is selected on the basis of its ability to evade the antibody response (Wei et al., 2003). We speculate that HIV-1 variants selected for their ability to evade antibodies due to lowered affinity will recall memory B cells to the germinal center for additional rounds of mutation and selection. Thus, iterative rounds of antibody mutation, selection, and viral escape would facilitate the accumulation of essential mutations in the FWR that conserve some key aspects of antibody structure while altering others to enhance anti-HIV-1 breadth and potency.

In conclusion our experiments suggest a molecular and a structural rationale for the requirement of high levels of somatic mutation found in broadly neutralizing antibodies and possibly for the observation that it takes several years for infected individuals to develop such antibodies. The high relevance of FWR mutations should be considered in the approach to designing an HIV-1 vaccine.

## Experimental procedures

### Sequence analysis of HIV-1-reactive antibodies

Analysis of heavy and light chain gene segment usage, number of somatic mutations, and the presence of deletions or insertions was carried out using the NCBI IgBLAST software (<http://www.ncbi.nlm.nih.gov/igblast/>). Complementarity determining regions (CDRs) and framework regions (FWRs) were designated according to the Kabat (Wu and Kabat, 1970) (Figure 1, Supplementary Data 1A–E and Table S1) or IMGT numbering system (Figure 1B and Supplementary Data 1F) using IgBLAST software. VRC01- and NIH45–46-FWR-GL<sup>CR+</sup> antibodies were designed to carry reverted FWRs with unreverted contact residues based on the crystal structure of a gp120-VRC01 complex (Zhou et al., 2010). 3BNC117- and 12A21-FWR-GL<sup>CR+</sup>-antibodies were based on the co-crystal structures as described by Peter Kwong and colleagues (Zhou et al., submitted). Any residue with a buried surface area (BSA) greater than 5 Å<sup>2</sup> was considered significant.

Sequences of the RU01 clone (Scheid et al., 2011) were aligned using Clustal V from the DNASTar package using PAM 250 matrix. The phylogenetic tree was constructed using the DNASTar package, which employs a neighbor joining method. Bootstrap values (1000 trials, seed=111) are as indicated (Figure 4). Classification of neutralization potency (RU01 clone)



was based on the neutralization activity. Antibodies were grouped into potent, intermediate and poor neutralizers by taking into account the potency ( $IC_{50}$ ) against BaL.26, DJ263.8, 6535.3, RHPA4259.7, Tro.11, PV0.4 and YU2.DG as well as breadth (number of the tested strains neutralized)(Scheid et al., 2011).

### Cloning, expression and purification of immunoglobulins

The variable regions of all mature, FWR-GL, FWR-GL<sup>CR+</sup> and CDR1/2 GL antibodies were cloned into the same IgH, Ig $\kappa$  or Ig $\lambda$  backbones encoding the constant domains of the antibodies. Reversions of the FWRs were introduced by overlapping polymerase chain reaction (PCR) or by DNA synthesis (Integrated DNA Technologies). The sequence of 17b was obtained from the structure with CD4 (pdb code 1G9M). The P61A mutation was introduced into the 3BNC60 heavy chain gene by site-directed mutagenesis using QuikChange Site-Directed Mutagenesis Kit (Agilent Technologies). Since the region of the FWR3 insertion is highly mutated and the exact location of inserted amino acids is difficult to determine, surrounding regions from 3BNC55 and 3BNC60 were included in each construct (Figure 5B). Likewise, the residues surrounding the engrafted insertion in VRC01 were chosen based on the crystal structures of VRC01 and 3BNC60 (Supplementary Data 1E) (Scheid et al., 2011; Zhou et al., 2010). Antibodies were expressed and purified as previously described (Mouquet et al., 2011) (Diskin et al., 2011).

### ELISA

ELISAs for analysing antibody-binding to gp140<sup>YU2</sup> (Figure 2, Figure 3 Figure S2) was performed as previously described (Mouquet et al., 2011).

### Neutralization assays

Neutralizing activities of mature, FWR-GL, FWR-GL<sup>CR+</sup>, and CDR1/2-GL antibodies were determined using a TZM.bl assay as previously described (Diskin et al., 2011; Li et al., 2005; Montefiori, 2005; Seaman et al., 2009). Briefly, TZM.bl cells were infected with different Tier 1 to Tier 3 HIV-1-Env-pseudoviruses in the presence of serial dilutions of the antibodies tested. Antibodies with neutralizing activity inhibit the infection and a reduction of luciferase reporter gene expression can be measured 48h after infection.  $IC_{50}$  values were calculated based on the antibody concentration that resulted in a 50% reduction of relative luminescence units (RLU).

### Surface plasmon resonance

Experiments were performed with a Biacore T200 (Biacore, Inc) as described previously (Diskin et al., 2011). Briefly, YU-2 gp140 was primary amine-coupled on CM5 chips (Biacore, Inc.) at an immobilization level of 1000 RUs. IgG antibodies were injected over flow cells at 1  $\mu$ M, at flow rates of 90  $\mu$ l/min. The sensor surface was regenerated by a 50 sec-injection of 10 mM glycine-HCl pH 2.5 at a flow rate of 90  $\mu$ l/min.

### Crystallization and structure of 3BNC60<sup>P61A</sup> Fab

3BNC60<sup>P61A</sup> Fab (pdb code 4GW4) was concentrated to 13.7 mg/ml in 20 mM Tris pH 8.0, 150 mM sodium chloride, 0.02% sodium azide (TBS) buffer. Crystals of Fab 3BNC60<sup>P61A</sup> were obtained by mixing a protein solution at 13.7 mg/ml with 16% polyethylene glycol 6000, 0.1 M citric acid pH 3.9, 0.15 M lithium sulfate monohydrate at 20°C. For cryoprotection, crystals were briefly soaked in mother liquor solutions supplemented with 15% and subsequently with 30% ethylene glycol before flash cooling in liquid nitrogen.

3BNC60<sup>P61A</sup> Fab crystals grew in space group  $P2_1$  ( $a = 64.6$ ,  $b = 154.9$ ,  $c = 74.2$  Å;  $\beta = 109.7^\circ$ ) and were isomorphous to 3BNC60 Fab crystals (Scheid et al., 2011). Data were

indexed, integrated and scaled using XDS (Kabsch, 2010). We used Phaser (McCoy et al., 2007) to find a molecular replacement solution for two Fabs per asymmetric unit (chains A and H and chains B and L for the heavy and light chains, respectively) using the 3BNC60 Fab structure (PDB code 3RPI) as a search model after omitting residues 59–66 of the heavy chain. Residues 59–66 were built into  $F_o - F_c$  difference electron density maps after a few rounds of iterative refinement including non-crystallographic symmetry restraints using Phenix (Adams et al., 2010) and Coot (Emsley et al., 2010). The final 2.65 Å resolution atomic model for two 3BNC60<sup>P61A</sup> Fabs ( $R_{\text{work}} = 21.5\%$ ;  $R_{\text{free}} = 25.6\%$ ) includes 12598 protein atoms (of which 6198 are hydrogen atoms), 199 water molecules, and 28 ligand atoms (N-acetylglucosamine attached to Asn70 of the light chain) (Table S3). Using the numbering established for the 3BNC60 Fab structure (Scheid et al., 2011), the residues included in the final model are 1–132 and 141–217 of chain H, 2–132 and 141–217 of chain A, 4–198 of chain L, and 4–199 of chain B. The first glutamine of the 3BNC60<sup>P61A</sup> heavy chain was modeled as 5-pyrrolidone-2-carboxylic acid. 94.5%, 5.3% and 0.3% of the residues were in the favored, allowed and disallowed regions of the Ramachandran plot, respectively.

### Thermal stability comparisons

Purified 3BNC60 and 3BNC60<sup>P61A</sup> Fabs were concentrated to 10 μM in 1 mM dithiothreitol, 5 mM sodium chloride for CD studies. Far UV wavelength scans (200 nm to 250 nm) were recorded in 1 nm increments using an averaging time of 5 seconds on an Aviv 62A DS spectropolarimeter. Both spectra showed a distinct negative signal at 218 nm, thus this wavelength was chosen for the thermal stability comparisons. Thermostability profiles were obtained by monitoring the CD signal at 218 nm as the temperature was raised from 40°C to 95°C in 2°C increments, allowing 1 min of equilibration time after each temperature step and averaging the CD signal over 30 sec of measurement. Transition midpoints ( $T_m$ ) were obtained by estimating the half-point of the ellipticity change between the native and denatured states.

### Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

### Acknowledgments

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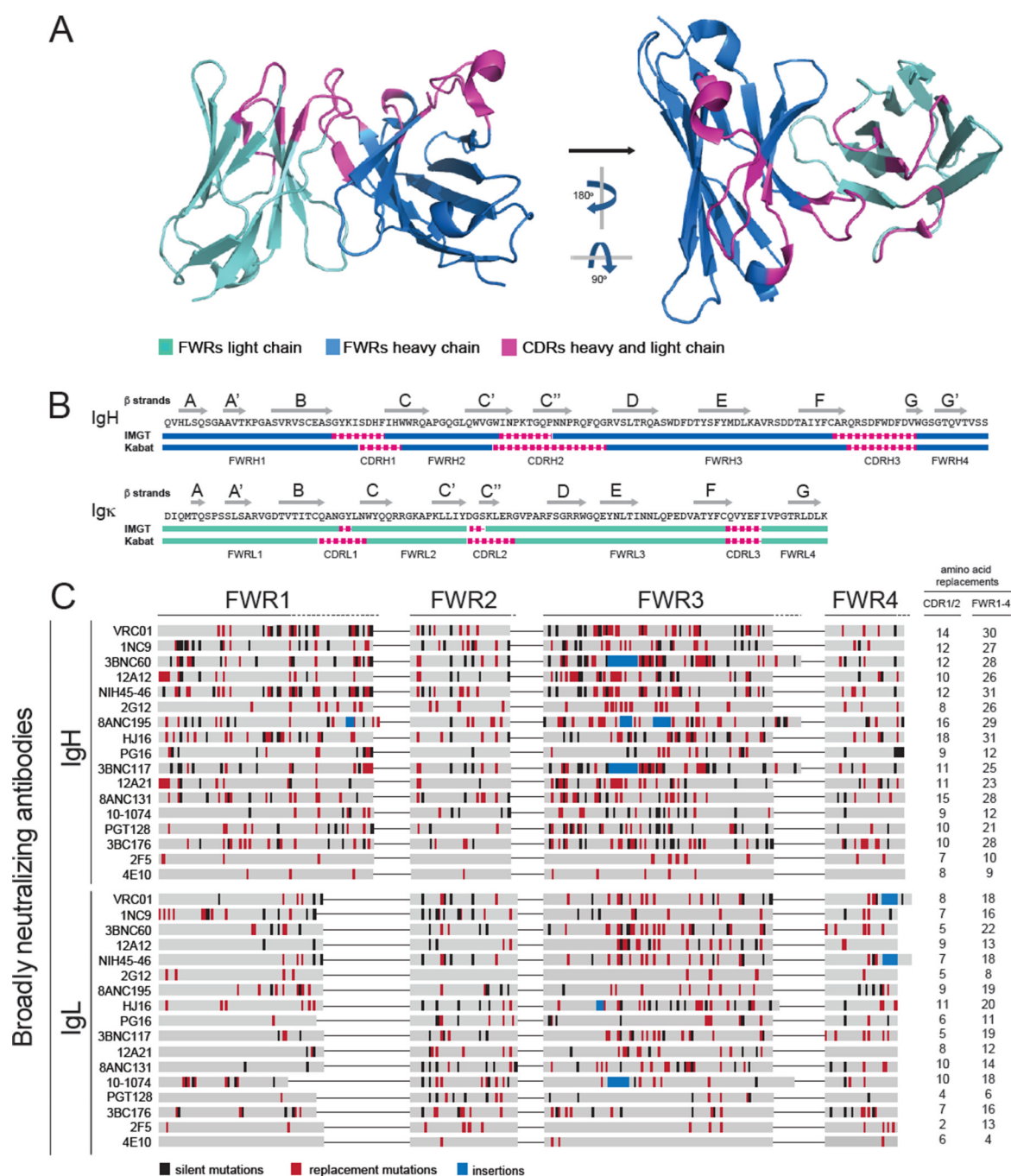
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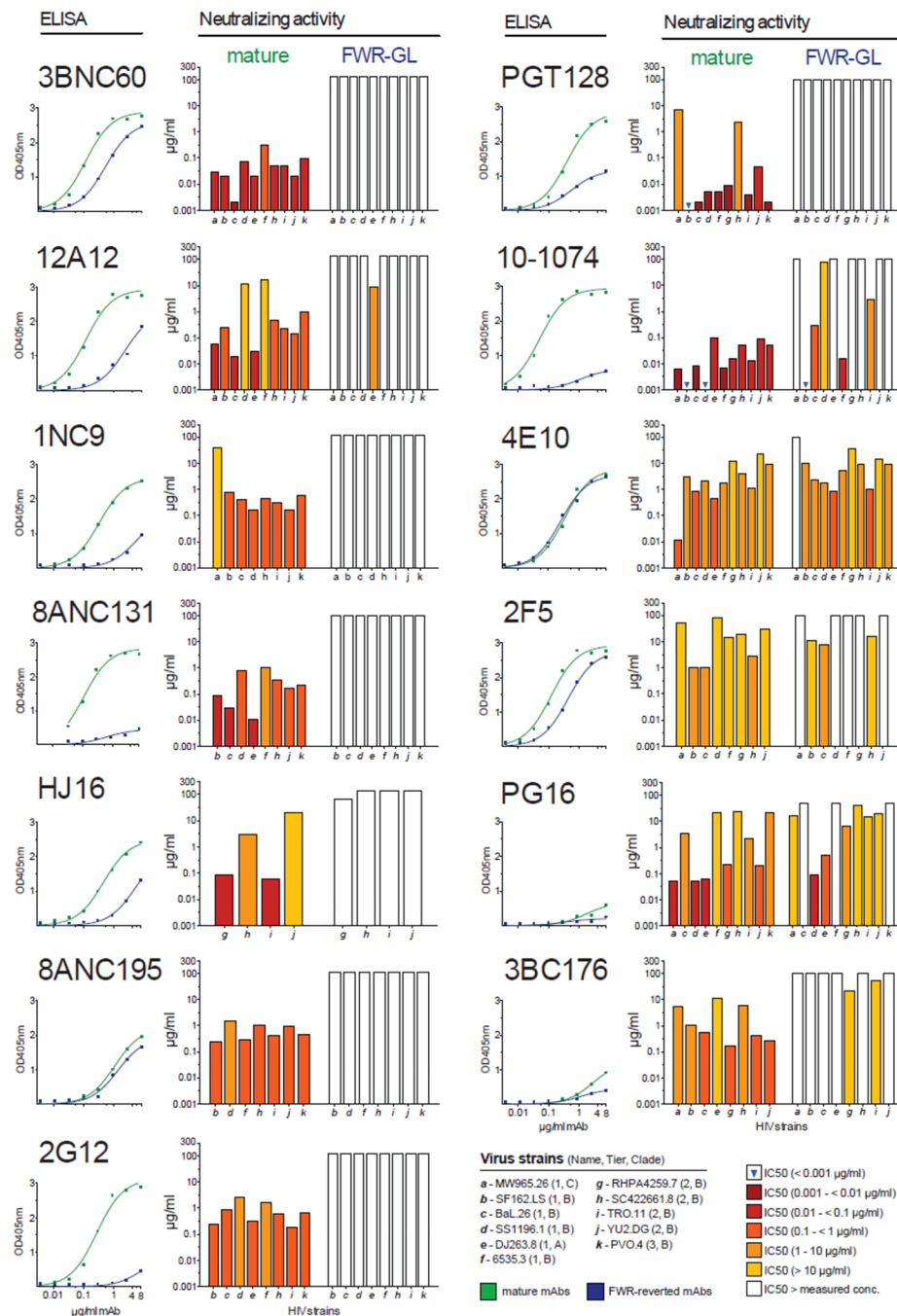
**Highlights**

- Framework mutations play a crucial role in broadly neutralizing HIV-1 antibodies



**Figure 1. Somatic mutations in the framework regions of HIV-1-reactive antibodies**  
**(A)** Ribbon representation of the variable domains of 3BNC60 (Scheid et al., 2011), illustrating the CDRs (magenta) and the FWRs of the immunoglobulin heavy (blue) and light (cyan) chain. **(B)** Illustration of Kabat and IMGT CDR (magenta) and FWR (IgH – blue; IgL – cyan) assignments for the variable heavy and light chain domains of 3BNC60. Gray arrows indicate  $\beta$ -strands defined by the crystal structure of the 3BNC60 Fab (Scheid et al., 2011). **(C)** Position of FWR mutations in heavy and light chain of the 17 investigated antibodies with broad neutralizing activity (see also Supplementary Data 1). Indicated are silent (black) and replacement (red) mutations. Insertions are illustrated in blue. Number of

replacement mutations within CDR1/2 and FWR1–4 are listed in the two columns at the very right (see also Table S1). HIV-1 reactive antibodies with limited neutralization are displayed in Figure S2.

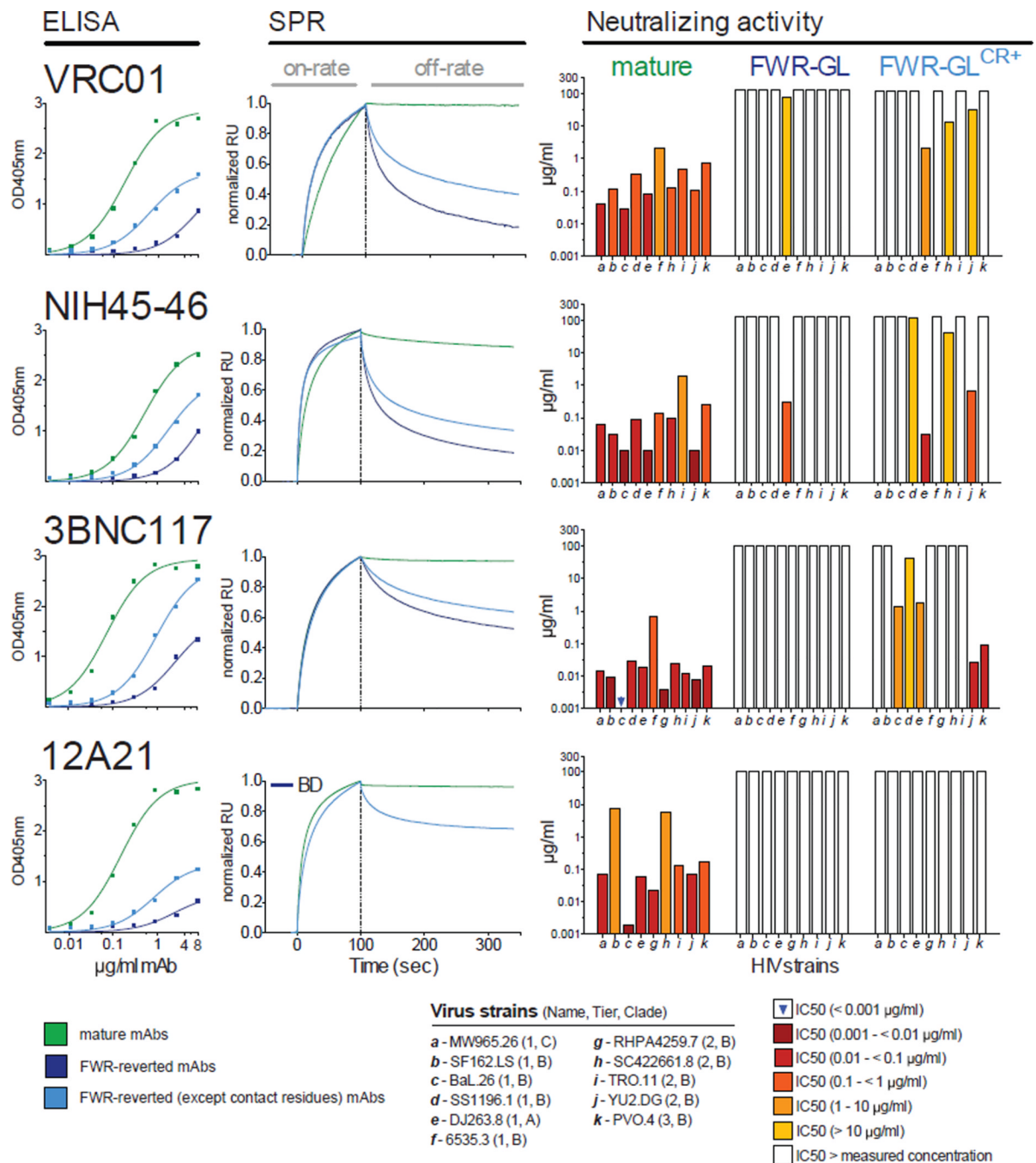


**Figure 2. Binding and neutralization activity of mature and FWR-reverted (FWR-GL) broad neutralizing antibodies**

Evaluation of binding to gp140<sup>YU2</sup> ELISA (left) of mature antibodies (green) and antibodies with FWRs reverted to germline (FWR-GL; blue, Supplementary Data 1B). Panels on the right compare IC<sub>50</sub> values for neutralization of Tier 1 (MW965.26, SF162.LS, Bal.26, SS1196.1, DJ263.8, 6535.3) Tier 2 (RHPA4259.7, SC422661.8, TRO.11, YU2.DG), and Tier 3 (PV0.4) viruses (Table S2). Only viruses are shown that were neutralized by the mature version of the antibody. Neutralization activity is color-coded (blue arrow: < 0.001 μg/ml; dark red: IC<sub>50</sub> between 0.001 and 0.01 μg/ml; red: > 0.01 – 0.1 μg/ml; orange: > 0.1 – 1 μg/ml; light orange: > 1 – 10 μg/ml; yellow: > 10 μg/ml; white: IC<sub>50</sub> was not achieved up

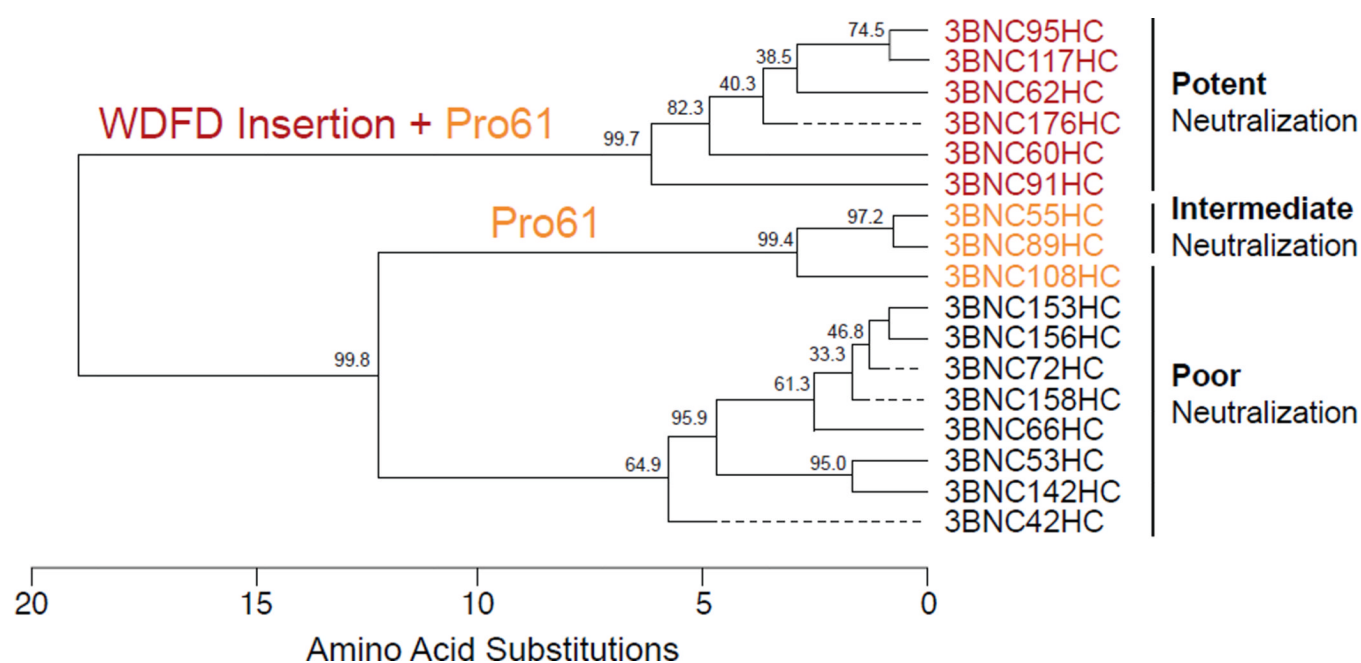


to the tested concentration). Antibodies (NIH45–46, 3BN60) with reverted CDR1/2 are shown in Figure S2A and HIV-1 reactive antibodies with limited neutralization are displayed in Figure S2B. The FWRs of VRC01, 3BNC60 and 3BNC131 were also reverted according to IMGT (Giudicelli et al., 2006) and results are shown in Figure S2C. A detailed illustration of the FWR mutations in 2G12 is shown in Figure S3.



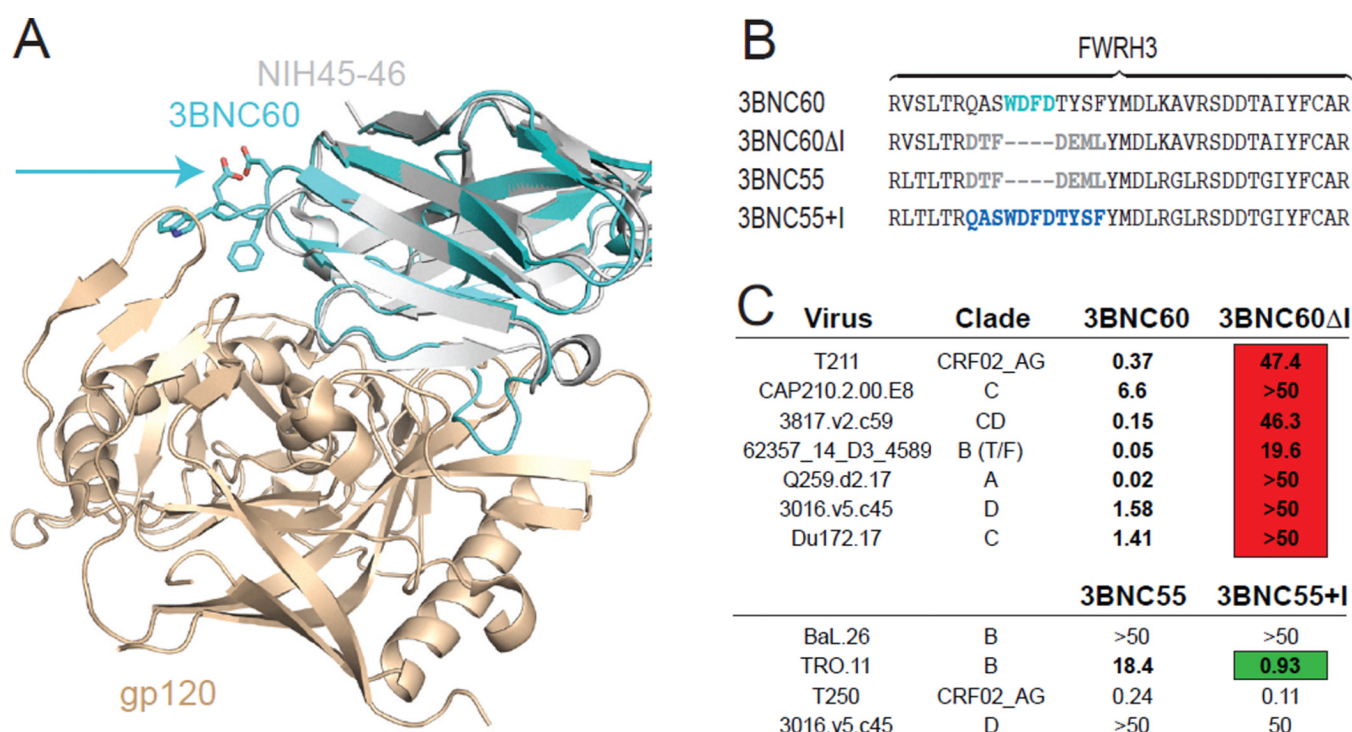
**Figure 3. Binding and neutralization activity of mature and FWR-reverted (FWR-GL and FWR-GL<sup>CR+</sup>) broad neutralizing antibodies**

Evaluation of binding to gp140<sup>YU2</sup> ELISA (left) and SPR (middle) of mature antibodies (green), antibodies with FWRs reverted to germline (FWR-GL, blue), and antibodies with germline-reverted FWRs except gp120-contacting residues (FWR-GL<sup>CR+</sup>; light blue; Supplementary Data ID). SPR results are shown for starting concentrations of 1 µM. BD (below detection; no binding of the antibody was observed). Panels on the right compare IC<sub>50</sub> values for neutralization of Tier 1 to Tier 3 viruses (Table S2) as in Figure 2. Neutralization activity is color-coded as indicated.



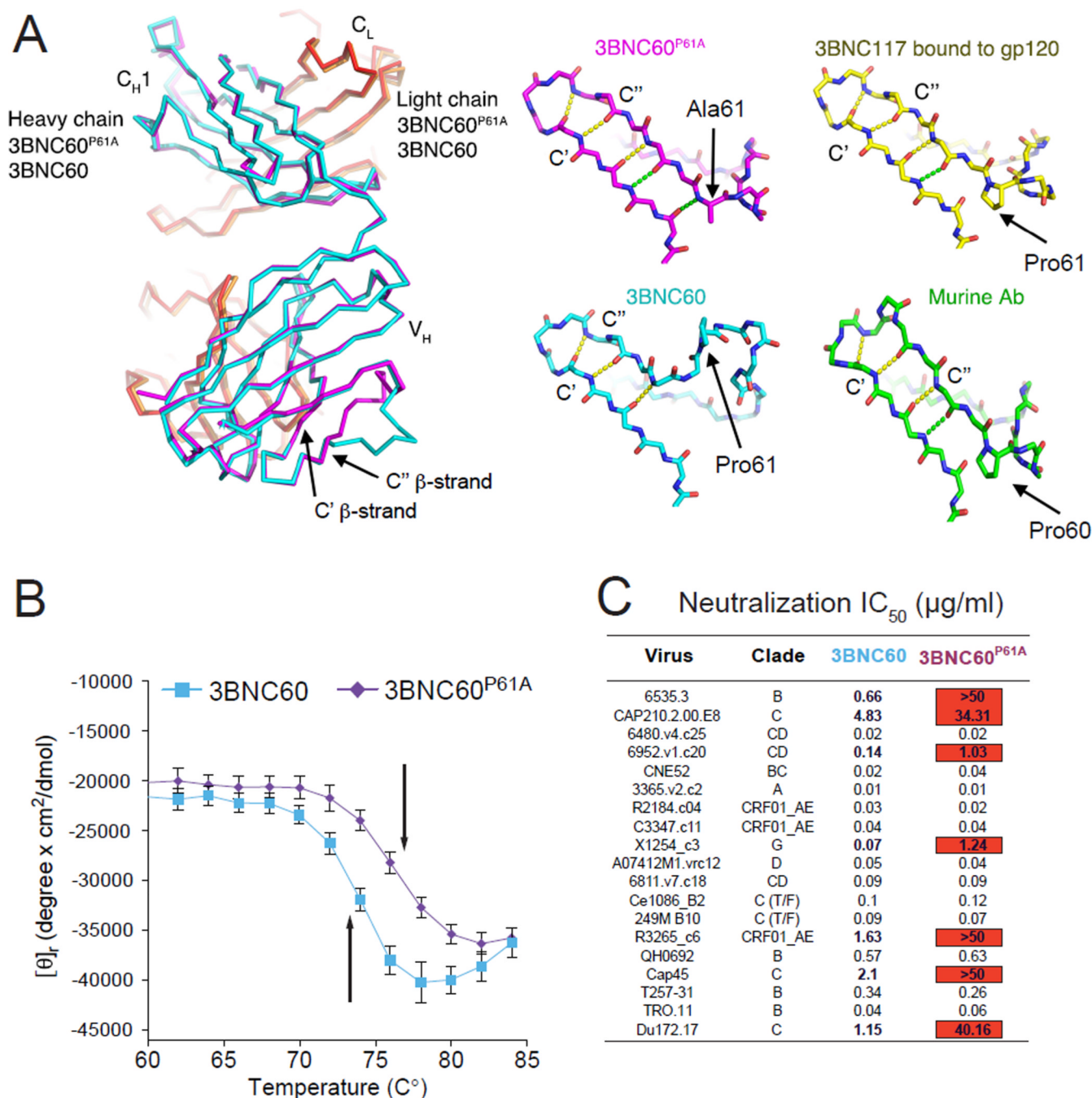
**Figure 4. Effects of a FWR insertion and a C''-strand proline in clone RU01**

Phylogenetic tree of the antibodies (Ig heavy chain) derived from the RU01 clone that members include 3BNC117 and 3BNC60 (Scheid et al., 2011). Antibodies that carry both the 4 amino acid insertion in FWR3 and the A61P somatic mutation are shown in red, antibodies with only the A61P mutation are shown in orange, and antibodies without either feature are shown in black. Bootstrap values (1000 trials, seed=111) of the phylogenetic tree are indicated. Structure of 3BNC117 IGVH in its gp120-bound conformation is shown in Figure S5.



**Figure 5. Analysis of 3BNC60 insertion**

(A) Superimposition of the structure of the V<sub>H</sub> domain of 3BNC60 (cyan) (Scheid et al., 2011) onto the NIH45–46 V<sub>H</sub> domain from cocrystal structure of NIH45–46 (gray) bound to gp120 (gold) (Diskin et al., 2011) highlighting the 4 residue insertion in FWR3 of 3BNC60 (cyan arrow) and a potential interaction between the insertion and the gp120 V1/V2 loop (note that the V1/V2 loop was truncated in the gp120 construct used for co-crystallization with NIH45–46 and VRC01) (Diskin et al., 2011; Zhou et al., 2010). (B) Alignment of the heavy chain FWR3 sequences of 3BNC60 (Scheid et al., 2011), 3BNC60 without the 3BNC60 insertion (3BNC60 ΔI), 3BNC55 (Scheid et al., 2011) and 3BNC55 containing the 3BNC60 insertion (3BNC55+I; Supplementary Data 1E). The 4 amino acid insertion in FWR3 of 3BNC60 is shown in cyan and the region grafted into 3BNC60 from 3BNC55 in order to delete the insertion without disrupting the structure is shown in gray. The amino acid changes to introduce the insertion into 3BNC55 are shown in cyan. (C) *In vitro* neutralization data (IC<sub>50</sub> values in μg/ml) comparing the potencies of the antibodies. The upper panel compares neutralization of selected viral strains by 3BNC60 and, 3BNC60 ΔI. The lower panel compares the neutralization by a less potent member of the RU01 clone (3BNC55), in which the FWR3 insertion of 3BNC60 was introduced (3BNC55+I). Reduced and increased neutralization activity of the engineered antibodies (3BNC60 ΔI, 3BNC55+I) is highlighted red and green, respectively. Neutralization data on VRC01 with and without the 3BNC60 insertion is displayed in Table S2.



**Figure 6. Comparison of 3BNC60 and 3BNC60<sup>P61A</sup> structures, thermal denaturation profiles and neutralizing activities**

(A, left) 3BNC60<sup>P61A</sup> (magenta heavy, chain; yellow, light chain) was superimposed on the structure of 3BNC60 (cyan, heavy chain; red, light chain; Table S3). The C''-strand within FWR3 of the V<sub>H</sub> domain differs in conformation between the two structures. (A, middle/right) Close-up of the C' and C''-strands of 3BNC60<sup>P61A</sup> (magenta), 3BNC117 bound to gp120 (yellow), 3BNC60 (cyan), and a murine Fab (green). The main chain atoms of the V<sub>H</sub> domain C' and C''-strands of 3BNC60<sup>P61A</sup> exhibit a typical hydrogen bonding pattern for an anti-parallel  $\beta$ -sheet. Three of the five inter-strand hydrogen bonds in 3BNC60<sup>P61A</sup> are found in all three structures (yellow dashed lines), whereas 3BNC60 lacks two and the



murine Fab/3BNC117 lacks one of the hydrogen bonds (green dashed lines in 3BNC60<sup>P61A</sup>). Co-crystallization of the 3BNC60-relative 3BNC117 with gpl20 shows that Proline61 is accommodated without disrupting the C' - C'' -sheet when 3BNC117 is bound to gpl20. Overview of the packing in crystals of 3BNC60 and 3BNC60<sup>P61A</sup> is shown in Figure S6. **(B)** Thermal denaturation profiles of the 3BNC60 and 3BNC60<sup>P61A</sup> Fabs monitored by the CD signal at 218 nm. T<sub>m</sub>S (indicated with arrows) were derived by estimating the halfpoint of the ellipticity change between the beginning and end of each transition. **(C)** *In vitro* neutralization data (IC<sub>50</sub> values in µg/ml) comparing the 3BNC60 and 3BNC60<sup>P61A</sup> IgGs for a panel of 19 viruses. Reduced neutralization activity is highlighted in red. Additional 9 viral strains (T250-4, T278-50, 620345.C01, X2088\_c9, 89-FI\_2\_25, 6540.v4.c1, CAP45.2.00.G3, 6545.v4.c1, Du422.1) were resistant to both 3BNC60 and 3BNC60<sup>P61A</sup>. The 3BNC60<sup>P61A</sup> mutant was not significantly more potent than 3BNC60 against any of the 27 strains tested.